We claim:

1. A method of constructing an apparatus for identifying a pathogenic agent in a sample, comprising

providing a set of host cells and contacting the cells with the pathogenic agent or any sample containing pathogenic agent,

employing a microarray having a plurality of probes to measure a plurality of biological responses of the host cells,

applying the measured plural biological responses to train a machine learning system to recognize a pathogenic agent, and

detecting and identifying a pathogenic agent in a sample, by exposing host cells to said sample, using a microarray to measure plural biological responses provoked in host cells, and employing the trained machine learning system to identify the pathogenic agent.

2. A method according to claim 1, further comprising

employing the set of host cells and a plurality of microarrays to increase a plurality of biological responses available to the identification process, and

applying machine learning to said plural biological responses to identify a pathogenic signature.

3. A method according to claim 2, further comprising

providing a plurality of sets of host cells,

contacting said host cells with a sample containing pathogenic agents to provoke and measure a plurality of biological responses,

training a recognizer to detect one or more of said pathogenic signatures in a biological response provoked in a host cell, and

applying machine learning to said plural respective biological responses to identify at least one pathogenic signature.

4. A method according to claim 1, further comprising

wherein the pathogenic agent to be identified is contained within an environmental sample that contains other substances and/or pathogenic agents.

5. A method according to claim 1, further comprising

employing substantially all of the measured biological response data during the identification method to widen the scope of information employed during pathogen detection.

6. A method according to claim 5, wherein

employing substantially all of the measured biological response data includes identifying a pathogen signature having substantially all of the measured biological data.

7. A method according to claims 1 and 3, further comprising

employing information fusion methods to allow recognition of pathogen identity.

8. A method according to claim 3, further comprising

allowing the recognizer to generate plural decision results, and

fusing said plural decision results to generate a determination of the identity of a pathogen in a test sample.

9. A method according to claim 1, further comprising

using the host cells as a natural amplification mechanism, wherein the host cell response to an agent of high virulence is vigorous, allowing improved detection and identification of pathogenic agents.

10. A method according to claim 1, further comprising

employing the similarity of the host cell response to pathogenic agents that represent different strains of the same pathogen, altered pathogens, genetically engineered pathogens, and/or mutated pathogens,

wherein the host cells act as a natural filtering mechanism allowing identification of the pathogenic agents that differ from the agents used for training

11. A method according to claim 1, wherein

employing a microarray includes employing a microarray having a uniform set of probes.

12. A method according to claim 1, wherein

employing a microarray includes employing microarrays of different modalities.

13. A method according to claim 12, wherein the different modalities include modalities selected from the group consisting of genomic, proteomic, and metabolomic.

14. A method according to claim 1, wherein the host cells include cultured host cells and/or host cells grown from cell lines.

15. A method according to claim 1, wherein the host cells include host cells of different types

16. A method according to claim 1, wherein host cells include cells selected from different organisms or species.

17. The method of claim 1, wherein the pathogenic agent is a non-nucleic-acid-containing pathogenic agent.

18. The method of claim 17, wherein the non-nucleic-acid-containing pathogenic agent is a toxin.

19. The method according to claim 1, wherein the pathogenic agent includes substances and/or stimuli capable of eliciting a response in the host cell.

20. The method of claim 1, wherein the sample is derived from a human or animal, and wherein the sample is selected from the group consisting of blood, urine, feces, sputum, saliva, semen, vaginal fluid, cerebrospinal fluid, skin cells, hair follicles, bone fragments, bone marrow, brain matter, and amniotic fluid.

21. The method of claim 1, wherein the sample is derived from an environmental or industrial matter.

22. The method of claim 1, wherein the sample consists of gas, liquid, or solid, or combinations of these states.

23. The method of claim 1, wherein the sample is selected from the group of air, water, and soil.

24. The method of claim 1, wherein the host cells comprise a cell selected from the group of lung, skin, nerve, and immune system.

25. The method of claim 1, wherein the one or more biological responses of the host cells comprise genomic microarray data of the host cell response.

26. The method of claim 1, wherein the one or more biological responses of the host cells comprise proteomic microarray data of the host cell response.

27. The method of claim 1, wherein the one or more biological responses of the host cells comprise both genomic microarray data and proteomic microarray data.

28. The method of claim 1, wherein the one or biological responses of the host cells comprise genomic, proteomic, metabolomic and fusion thereof.

29. The method of claim 1, wherein the microarrays include microarrays having non-uniform probe sets, or multiple microarrays having different sets of probes.

30. A method of claim 1, further comprising

fusing information from multiple types and/or species of host cells, multiple microarray types, multiple and/or disparate sets of probes, and/or multiple modalities.

31. A method of claim 1, further comprising

fusing multiple candidate identification responses to generate a fused identification.

32. A method of claim 1, further comprising

fusing multiple candidate identification responses generated by multiple classifiers.

33. The method of claim 1, further comprising

partitioning an input space of microarray probes into one or more computational subspaces and generating measures of fitness for said subspaces.

34. The method of claim 1, further comprising

generating multiple measures of fitness within a subspace wherein intra-subspace measures of fitness are dynamic having a value depending on the region within the subspace and position within the subspace of a point representing the test sample

35. The method of claim 7,

wherein fusing includes weighting candidate identification responses.

36. A method for identifying the presence of a pathogenic agent, comprising

collecting disparate types of biological data representative of a biological response to the same pathogenic agent, and

employing information fusion to process the biological response.

37. The method of claim 36, including the further step of

collecting multiple modalities of biological data representative of a biological response to the same pathogenic agent.

38. The method of claim 36, wherein collecting data includes employing microarrays having a set of probes.

39. The method of claim 36, further comprising applying machine learning to process the biological data and to develop a signature for the pathogen that includes substantially all of the data collected by common probes among the microarrays.

40. The method of claim 36, wherein

the biological response include the biological response of a host cell.

41. A pathogenic agent signature, comprising the data set generated by the method of claim 1.

42. The method of claim 1, further comprising determining for a subspace a fitness measure representative of an effectiveness of a classifier operating in the respective sub-space.

43. The method of claim 1, wherein analyzing a data set includes partitioning an input space into plurality of subspaces.

44. The method of claim 1, further comprising fusing measures of recognition generated from respective areas of said sub-spaces.

45. The method of claim 44, further comprising using sub-space measures of fitness and fusing multiple classifiers.

46. The method of claim 1, further comprising
applying Dempster-Shafer theory of evidence for fusing multiple classifiers.